October 2, 2009

Examiner Bin Shen
USPTO

Re: Interview Agenda for Application Serial No: 10/568,215

Examiner Shen:

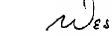
Thank you for agreeing to schedule a telephonic interview involving you, Examiner Weber, and myself to discuss the patentable subject matter of Application Serial No: 10/568,215.

I propose we discuss possible language amendments to independent claims 1 and 15 as applied to the cited prior art of Wagner et al., Gygi et al., and Kachman et al. In particular, I propose we discuss language to clarify the simultaneous multidimensional aspects of the subject invention that are neither taught nor suggested by the cited prior art.

Please see the PROPOSED amendments attached to this communication that Applicant submits fully address the outstanding rejections under 35 U.S.C. §112, second paragraph.

I look forward to speaking with you.

Best regards,



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Enclosure

Proposed Amendments to the Claims

1. **[Proposed Amended]** A process for analyzing proteins or viruses in a sample comprising:
dividing a sample having a protein or virus component into a plurality of aliquots;
applying said plurality of aliquots in parallel to a plurality of simultaneous different first separation steps to yield a plurality of uniquely different partially resolved eluates;
subjecting said plurality of partially resolved eluates in parallel to a second separation step to yield a plurality of resolved fractions, and
characterizing the protein or virus composition of ~~analyzing~~ at least one of said plurality of resolved fractions. **[0019]**

2. (Previously Presented) The process of claim 1 further comprising collecting at least one of said plurality of resolved fractions.

3. (Original) The process of claim 2 wherein collection of the at least one of said plurality of resolved fractions occurs onto a MALDI target or plate.

4. (Canceled) The process of claim 1 further comprising the step of analyzing at least one of said plurality of resolved fractions.

5. **[Proposed Amended]** The process of claim [[4]] 1 wherein analysis is by mass spectrometry.

6. (Original) The process of claim 5 wherein said mass spectrometry is performed on a MALDI mass spectrometer.

7. (Previously Presented) The process of claim 3 further comprising the step of analyzing at least one of said plurality of resolved fractions by mass spectrometry wherein said mass spectrometry is performed on an orthogonal MALDI mass spectrometer.

8. (Original) The process of claim 1 wherein at least one of said first and said second separation steps separate on a basis selected from the group consisting of: charge, molecular weight, and hydrophobicity.

9. (Original) The process of claim 1 wherein at least one of said first and said second separation steps uses a chromatography resin or chromatography membrane.

10. (Original) The process of claim 1 wherein at least one of said first and said second separation steps comprises a separation buffer that varies monotonically between individual aliquots or individual eluates.

11. (Original) The process of claim 1 wherein at least one of said first and said second separation steps comprises a separation matrix in linear or two-dimensional array.

12. (Original) The process of claim 11 wherein said first and said second separation steps occur with matrices maintaining well addresses in each of the two matrices.

13. (Original) The process of claim 1 wherein at least one of said first or said second separation steps occurs within a microplate.

14. (Previously Presented) The process of claim 1 further comprising: digesting said plurality of partially resolved eluates prior to subjecting said plurality of partially resolved eluates in parallel to said second separation step.

15. **[Proposed Amended]** A process for analyzing proteins or viruses in a sample comprising:

dividing a sample having a protein or virus component into a plurality of aliquots;

applying said plurality of aliquots in parallel to a plurality of simultaneous different first separation steps to yield a plurality of uniquely different partially resolved eluates;

subjecting said plurality of partially resolved eluates in parallel to a second separation step to yield a plurality of resolved fractions;

digesting said plurality of partially resolved eluates with a proteolytic enzyme to yield a plurality of digested eluates;

subjecting said plurality of digested eluates in parallel to a second separation step to yield a plurality of resolved peptide fractions, and

characterizing the protein or virus composition of ~~analyzing~~ at least one of said plurality of resolved fractions. **[0019]**

16. (Previously Presented) The process of claim 15 further comprising: collecting at least one of said plurality of resolved fractions.

17. (Original) The process of claim 16 wherein collection of the at least one of said plurality of resolved fractions occurs onto a MALDI target or plate.

18. (Canceled) The process of claim 15 further comprising analyzing at least one of said plurality of resolved fractions.

19. **[Proposed Amended]** The process of claim [[18]] 15 wherein analysis is by mass spectrometry.

20. (Canceled)

21. (Original) The process of claim 19 wherein said mass spectrometry is performed on an orthogonal MALDI mass spectrometer.

22. (Original) The process of claim 15 wherein at least one of said first and said second separation steps separate on a basis selected from the group consisting of: charge, molecular weight, and hydrophobicity.

23. (Canceled)

24. (Original) The process of claim 15 wherein at least one of said first and said second separation steps comprises a separation buffer that varies monotonically between individual aliquots or individual eluates.

25. (Original) The process of claim 15 wherein at least one of said first and said second separation steps comprises a separation matrix in linear or two-dimensional array.

26. (Original) The process of claim 25 wherein said first and said second separation steps occur with matrices maintaining well addresses in each of the two matrices.

27. (Original) The process of claim 15 wherein at least one of said first or said second separation steps occurs within a microplate.

28. (Canceled)

29. (Canceled)

30. **[Proposed Amended]** The process of claim [[18]] 15 further comprising analyzing at least one of said plurality of partially resolved eluates prior to digestion in concert with the corresponding resolved fraction.

31. (Original) The process of claim 30 wherein analysis is by mass spectrometry.

32. (Previously Presented) The process of claim 1 wherein the step of applying said plurality of aliquots in parallel to said first separation step is performed by a robot.

33. (Previously Presented) The process of claim 1 further comprising affixing a machine-readable label to at least one collection selected from the group consisting of: said plurality of aliquots, said plurality of partially resolved eluates, and said plurality of resolved fractions.

34. (Previously Presented) The process of claim 1 further comprising the steps of:
labeling a subsample with a unique tag; and
combining said subsample with a second uniquely labeled subsample or an unlabeled subsample prior to said plurality of aliquots.

35-42. (Canceled)